

AP20 Rec'd PCT/PTO 13 JUL 2006

NEB-236-PCT.ST25.txt
SEQUENCE LISTING

<110> New England Biolabs, Inc.
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Kumar, Sanjay
Kucera, Rebecca

<120> Modulation of Enzyme Activity by Changing Reciprocal Stereo-Geometric Positions of Two Catalytic Centers in an Enzyme

<130> NEB-236-PCT

<150> 60/524,123
<151> 2003-11-21

<160> 25

<170> PatentIn version 3.2

<210> 1
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gtgccttatg taattccggc gagcaatcac acttacactc cagacttctt acttccaaac 180
ggtatattcg ttgagacaaa gggctctgtgg gaaagcgatg atagaaagaa gcacttatta 240
attagggagc agcaccggc gctagacatc cgtattgtct tctcaagctc acgtactaag 300
ttatacaaag gttctccaac gtcttatgga gagttctgcg aaaagcatgg tattaagttc 360
gctgataaac tgataacctgc tgagtggata aaggaaccca agaaggaggt ccccttgat 420
agattaaaaa ggaaaggagg aaagaataaa 450

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<220>
<223> primer

<400> 2
cccgaaattca tggcagggtta cggcgct 27

<210> 3
<211> 27
<212> DNA
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<220>

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<223> primer
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cccccaagct tatttctttc ctccttt 27

<210> 4
<211> 30
<212> DNA
<213> unknown

<220>
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tggaagtaag aagtctggcc actcttcata 30

<210> 5
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<212> DNA
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<220>
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ttcgagttatg aagagtggcc agacttctta 30

<210> 6
<211> 39
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<220>
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aaagtgcctt atgttaattgc gagcaatcac acttacact 39

<210> 7
<211> 39
<212> DNA
<213> unknown

<220>
<223> oligonucleotide
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agtgttaagtg tgattgcacg caattacata aggcaacttt 39

<210> 8
<211> 36
<212> DNA
<213> unknown

<220>
<223> oligonucleotide
<400> 8

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aaagtgcctt atgtaattag caatcacact tacact

36

<210> 9
<211> 36
<212> DNA
<213> unknown

<220>
<223> oligonucleotide

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36

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<211> 40
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<213> unknown

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<223> oligonucleotide mixture

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<222> (24)..(24)
<223> n is a, c, g, or t

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aaagtgcctt atgtaaattc ccantaatca cacttacact

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<211> 40
<212> DNA
<213> unknown

<220>
<223> oligonucleotide mixture

<220>
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<222> (17)..(17)
<223> n is a, c, g, or t

<400> 11
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40

<210> 12
<211> 149
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<213> unknown

<220>
<223> enterobacteria phage T7

<400> 12

Met Ala Gly Tyr Gly Ala Lys Gly Ile Arg Lys Val Gly Ala Phe Arg
1 5 10 15

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Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
35 40 45

Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
50 55 60

Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
65 70 75 80

Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
85 90 95

Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
100 105 110

Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
115 120 125

Trp Ile Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys Arg
130 135 140

Lys Gly Gly Lys Lys
145

<210> 13
<211> 151
<212> PRT
<213> unknown

<220>
<223> yersinia pestis phage phiA1122

<400> 13

Met Ala Gly Thr Tyr Ala Ala Arg Gly Ile Arg Lys Val Gly Thr Phe
1 5 10 15

Arg Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Gly Lys Gly
20 25 30

Ile Lys Phe Asp Tyr Glu Leu Trp Lys Ile Pro Tyr Val Val Pro Ala
35 40 45

Ser Asn His Val Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
50 55 60

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Ile Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu
65 70 75 80

Leu Ile Arg Glu Gln Phe Pro Glu Leu Asp Ile Arg Leu Val Phe Ser
85 90 95

Ser Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu
100 105 110

Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
115 120 125

Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys
130 135 140

Gln Ala Lys Gly Gly Lys Lys
145 150

<210> 14
<211> 153
<212> PRT
<213> unknown

<220>
<223> bacteriophage phiYe03-12

<400> 14

Met Ala Gly Ala Tyr Ala Ala Arg Gly Val Arg Lys Val Gly Ala Phe
1 5 10 15

Arg Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly
20 25 30

Ile Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Ala
35 40 45

Ser Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
50 55 60

Ile Glu Thr Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu
65 70 75 80

Leu Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser
85 90 95

Ser Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Ala Glu
100 105 110

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Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
115 120 125

Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys
130 135 140

Thr Lys Lys Gly Val Lys Lys Asn Gly
145 150

<210> 15
<211> 152
<212> PRT
<213> Bacteriophage T3

<400> 15

Met Ala Gly Ala Tyr Ala Ala Arg Cys Thr Gln Gly Arg Ala Phe Arg
1 5 10 15

Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Glu Ser
35 40 45

Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Ile
50 55 60

Glu Thr Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu Leu
65 70 75 80

Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser Ser
85 90 95

Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Trp
100 105 110

Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val Ala
115 120 125

Gly Val Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys Thr
130 135 140

Lys Lys Gly Val Lys Lys Asn Gly
145 150

<210> 16
<211> 147
<212> PRT
<213> unknown

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<220>

<223> pseudomonas phage gh-1

<400> 16

Met Ala Tyr Ala Gly Pro Lys Gly Ala Arg Thr Gly Ala Phe Arg Ser
1 5 10 15

Gly Leu Glu Asp Arg Asn Ala Lys His Met Asp Lys Leu Gly Val Lys
20 25 30

Tyr Asp Phe Glu Arg Phe His Ile Asn Tyr Val Val Pro Ala Arg Asp
35 40 45

Ala Lys Tyr Thr Pro Asp Phe Val Leu Ala Asn Gly Ile Ile Ile Glu
50 55 60

Thr Lys Gly Ile Trp Glu Val Asp Asp Arg Lys Lys His Leu Leu Ile
65 70 75 80

Arg Glu Gln Tyr Pro Asp Leu Asp Ile Arg Leu Val Phe Ser Asn Ser
85 90 95

Asn Ser Lys Ile Tyr Lys Gly Ser Pro Thr Ser Tyr Ala Asp Phe Cys
100 105 110

Thr Lys His Gly Ile Gln Phe Ala Asp Lys Leu Val Pro Arg Asp Trp
115 120 125

Leu Lys Glu Ala Arg Lys Glu Ile Pro Gln Gly Val Leu Val Pro Lys
130 135 140

Lys Gly Gly
145

<210> 17

<211> 141

<212> PRT

<213> unknown

<220>

<223> pseudomonas putida KT2440

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Met Gly Leu Lys Tyr Gly Phe Arg Ser Gly Leu Glu Glu Arg Ala Ala
1 5 10 15

Asp Gln Leu Thr Ala Val Gly Met Gly Phe Thr Phe Glu Ser Leu Val
20 25 30

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Val Pro Tyr Thr Arg Pro Ala Lys Val His Lys Tyr Thr Pro Asp Phe
35 40 45

Ala Leu Ala Asn Gly Ile Ile Val Glu Thr Lys Gly Arg Phe Leu Thr
50 55 60

Glu Asp Arg Gln Lys Gln Leu Leu Val Lys Ala Gln His Pro Glu Leu
65 70 75 80

Asp Val Arg Phe Val Phe Ser Asn Ser Lys Thr Lys Ile Asn Lys Arg
85 90 95

Ser Thr Thr Thr Tyr Ala Asp Trp Cys Ser Lys Asn Gly Phe Gln Tyr
100 105 110

Ala Asp Lys Leu Val Pro His Ala Trp Leu Asn Glu Pro Val Asn Glu
115 120 125

Ala Ser Leu Ser Ile Ile Lys Gly Leu Ser Lys Glu Lys
130 135 140

<210> 18
<211> 134
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<220>
<223> roseophage SI01

<400> 18

Met Leu Asn Ser Lys Ser Ser Thr Arg Lys Arg Ala Leu Lys Ala Gly
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Tyr Arg Ser Gly Leu Glu Glu Gln Thr Ala Lys Asp Leu Lys Lys Arg
20 25 30

Lys Val Leu Phe Thr Tyr Glu Glu Thr Lys Ile Lys Trp Leu Asp Ser
35 40 45

Lys Val Arg Thr Tyr Thr Pro Asp Phe Val Leu Pro Asn Gly Val Ile
50 55 60

Ile Glu Thr Lys Gly Arg Phe Val Ala Ala Asp Arg Arg Lys His Leu
65 70 75 80

Glu Ile Gln Lys Gln Phe Gly Thr Leu Tyr Asp Ile Arg Phe Val Phe
85 90 95

NEB-236-PCT.ST25.txt

Thr Asn Ser Lys Ala Lys Leu Tyr Lys Gly Ala Lys Ser Ser Tyr Ala
100 105 110

Asp Trp Cys Asn Lys His Gly Phe Leu Tyr Ala Asp Lys Thr Ile Pro
115 120 125

Glu Asp Trp Leu Asn Glu
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<212> DNA
<213> unknown

<220>
<223> artificial

<220>
<221> misc_feature
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aattcccaagt a

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<210> 21
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<212> DNA
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<223> synthetic

<220>
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<222> (9)..(9)
<223> mismatch

<220>

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<221> misc_feature
<222> (15)..(15)
<223> mismatch

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aattcccaagt accaataatc 20

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<220>
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<222> (9)..(9)
<223> mismatch

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<212> DNA
<213> unknown

<220>
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<220>
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<222> (9)..(9)
<223> mismatch

<220>
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<222> (13)..(13)
<223> mismatch

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<220>
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Met Ala Gly Tyr Ser Ala Lys Gly Ile Arg Lys Val Gly Ala Phe Arg
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NEB-236-PCT.ST25.txt

Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
35 40 45

Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
50 55 60

Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
65 70 75 80

Ile Arg Lys Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
85 90 95

Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
100 105 110

Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
115 120 125

Trp Ile Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys Arg
130 135 140

Lys Gly Gly Lys Lys
145

<210> 25
<211> 149
<212> PRT
<213> unknown

<220>
<223> enterobacteria phage T7

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Met Val Gly Tyr Gly Val Lys Gly Ile Arg Lys Val Gly Ala Phe Arg
1 5 10 15

Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
35 40 45

Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
50 55 60

Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
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65

70

75

80

Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
85 90 95

Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
100 105 110

Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
115 120 125

Trp Ile Lys Glu Pro Lys Lys Glu Val Ser Phe Asp Arg Leu Lys Arg
130 135 140

Lys Gly Gly Lys Lys
145